Proposed synopsis on

DEEP LEARNING APPROACHES FOR EARLY DETECTION AND CLASSIFICATION OF BLOOD CANCER

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Deep Learning Approaches for Early Detection and Classification of Blood Cancer

1. Introduction

Medical science and diagnostic technology have witnessed numerous developments in recent years. Moreover, there has been a major increase in the number of diseases that may be monitored and aided by machines. One of those is blood cancer. Blood cancer is also known as hematologic cancer, which encompasses a group of malignancies that affect the blood, bone marrow, and lymphatic system [1][2]. Common types include leukaemia, lymphoma, and myeloma, each characterized by abnormal cell growth and function within these vital components of the circulatory and immune systems [3][4]. Early detection and accurate classification of blood cancer are critical for timely intervention and personalized treatment strategies [5][6]. Figure 1 represents a diagrammatic view of cancer stages and its symptoms.

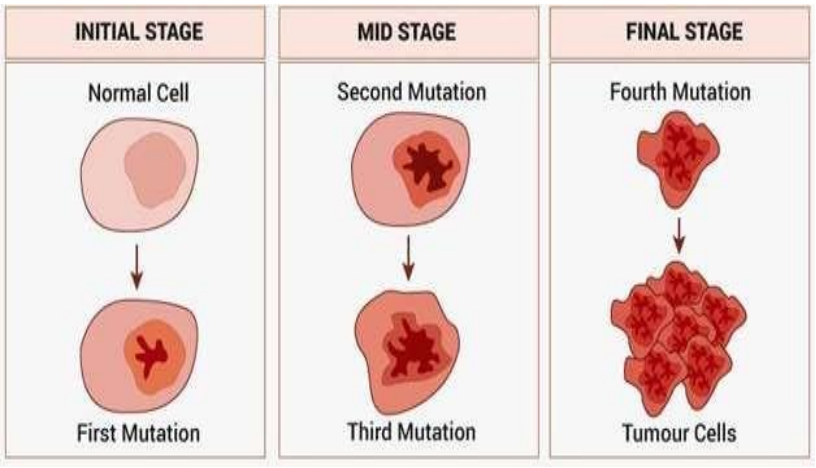

Figure 1. Blood cancer symptoms by biological tests [7].

Blood cancer originates from genetic mutations in blood cells, disrupting their normal growth and function [8][9][10]. Leukaemia involves the rapid production of abnormal white blood cells, while lymphoma affects lymphocytes (a type of white blood cell) and could develop in lymph nodes, spleen, or bone marrow [11][12]. Myeloma involves malignant plasma cells in the bone marrow, leading to weakened bones and impaired immune function [13][14]. Symptoms vary but

might include fatigue, bruising, recurrent infections, and swollen lymph nodes [15]. Figure 2 represents the symptoms that appear in a patient affected by cancer.

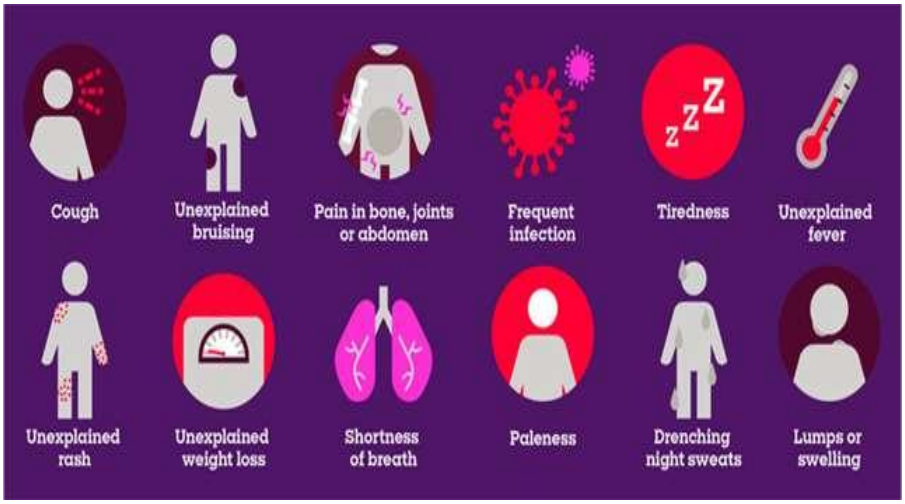

Figure 2. Morphological symptoms of blood cancer [16]

Cancer treatment with such symptoms and vast categorization encompasses a range of strategies such as surgery, chemotherapy, radiation therapy, immunotherapy, and targeted therapy. These interventions are tailored to individual patients based on cancer type, stage, and other factors [7]. Combining multiple modalities helps to effectively eradicate cancer cells, manage symptoms, and enhance overall survival rates. Figure 3 shows the treatment for blood cancer.

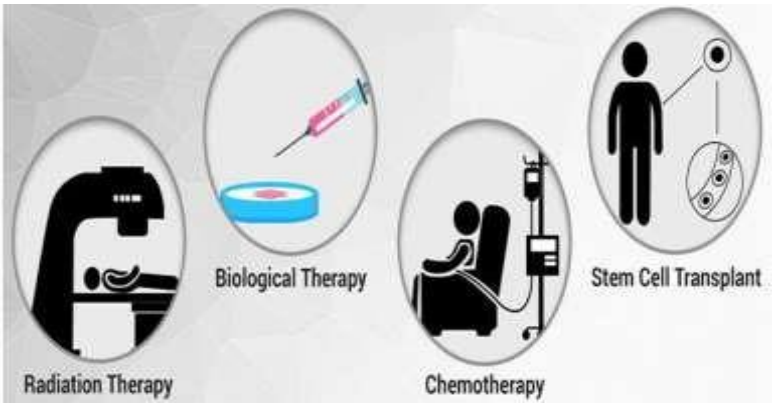

Figure 3. Blood cancer treatments [7].

Deep learning algorithms in the field of blood cancer utilize features derived from blood cell pictures or genetic data to identify abnormalities that are symptomatic of particular types of cancer [17][18]. Deep learning (DL), a subset of machine learning (ML), has gained traction in medical

diagnostics due to its ability to analyze complex patterns in large datasets [19][20]. These approaches aim to automate and enhance the accuracy of cancer diagnosis, offering the potential for earlier detection and intervention [21][22].

Several pre-developed deep-learning approaches target the early detection and classification of blood cancer [23][24]. Convolutional neural networks (CNNs) are commonly used for image analysis of blood smears to identify abnormal cells indicative of leukaemia or lymphoma [25][26]. Recurrent neural networks (RNNs) are employed for genetic sequence analysis to detect mutations associated with certain blood cancers [27][28]. Transfer learning techniques, leveraging pre-trained models, enable effective adaptation to medical imaging datasets with limited labelled samples [29][30]. Despite their promise, pre-developed deep-learning models for blood cancer detection face challenges [31]. Limited annotated datasets hinder model generalization and performance across diverse patient populations [32][33]. Interpretability remains a concern, as black-box deep learning models might obscure the rationale behind diagnostic decisions [34]. Furthermore, model robustness to variations in sample quality and disease presentation requires further validation and refinement.

Challenges in advancing deep learning approaches for blood cancer detection include:

- Data Quality and Quantity: Access to large, diverse, and well-annotated datasets is essential for training robust models [35].
- Interpretability: Developing explainable AI techniques to enhance trust and adoption of deep learning-based diagnostic tools [36].
- Clinical Validation: Conducting rigorous clinical trials to validate the performance and impact of deep learning models in real-world healthcare settings [37].
- Integration into Clinical Workflow: Ensuring seamless integration of AI-driven diagnostics into existing clinical workflows while addressing regulatory and ethical considerations [38].

Leveraging deep learning for early detection and classification of blood cancer holds immense potential to transform clinical practice. Overcoming challenges related to data quality, model interpretability, and clinical validation is imperative for harnessing the full benefits of these innovative technologies in improving patient outcomes and advancing precision medicine in hematology.

2. Motivation and Scope

Research on deep learning approaches for early detection and classification of blood cancer is motivated by the urgent need to improve patient outcomes through timely diagnosis and personalized treatment. Blood cancers, such as leukaemia and lymphoma, are diverse and complex diseases with varying genetic signatures and clinical presentations. Early detection using conventional methods could be challenging due to subtle symptoms and overlapping features with benign conditions.

Deep learning offers the potential to analyze large-scale biomedical data, including imaging and genomic sequences, to identify subtle patterns indicative of specific blood cancer types. The scope of the research includes developing accurate and interpretable deep learning models, integrating them into clinical workflows for real-time diagnostics, and ensuring scalability and generalizability across diverse patient populations. The ultimate goal is to leverage AI-driven technologies to enable earlier detection, precise classification, and tailored therapeutic strategies, thereby improving survival rates and quality of life for individuals with blood cancer. The research contributions for this study are as follows:

- The study contributes to automating the classification of different blood cancer types based on subtle image features, reducing the reliance on manual interpretation and potentially aiding in faster diagnosis.
- The study explores the scalability and generalization of deep learning models for blood cancer detection across diverse datasets and patient populations, enhancing the model's robustness and applicability in real-world clinical settings.
- This research contributes to advancing the field of digital pathology and computer-aided diagnosis, paving the way for more sophisticated and accurate diagnostic tools in healthcare.

3. Review of literature

This part provides a thorough overview and analysis of previous research, laying the foundation for the current investigation. The authors' prior research is presented in the related work section's structure.

3.1 ML and DL techniques for blood cancer detection

In 2024, **Abbasi et al. [39]** introduced the diagnosis of leukaemia via the precise analysis of multi-omics data using algorithms grounded on machine learning along with deep learning. While Recurrent Neural Networks (RNNs) achieved 98% accuracy in deep learning (DL), Gradient Boosting (GB) only managed 97% accuracy in machine learning (ML).

In 2024, **Perveen et al. [40]** proposed a web-based platform that classifies hematogone occurrences according to their Acute lymphoblastic leukemia (ALL) status using a Residual Convolutional Neural Network (ResNet-152) as its foundational learner and a weighted ensemble learning strategy. In the end, the proposed platform achieved respectable levels of F1-Score (99.90%), sensitivity (99.92%), recall (99.92%), specificity (99.97%), accuracy (99.95%), and precision (99.92%).

In 2021, **Amin et al. [41]** presented a deep learning technique via an open neural network exchange (ONNX) and you only live once (YOLO)v2 for detecting of leukaemia. The ALL-IDB1 dataset had a classification accuracy of 99.57%, the ALL-IDB2 dataset had 98.25%, and the LISC datasets had 98.4% accuracy using the optimizable support vector machine (SVM) kernel.

In 2021, **Sahaai et al. [42]** proposed a DNN design for tumor localization identification that utilizes stacked auto-encoders. Brain tumors' Magnetic resonance imaging (MRI) scans serve as both training and testing data for the suggested model. By re-mapping the histogram with updated pixel values, histogram equalization raises the contrast of a grayscale picture. A sum of 93.7 points for Precision, 87.8 for Specificity, 95.3 for Accuracy, and 94.6 for F1-Score were the outcomes.

In 2020, **Loey et al. [43]** introduced two transfer-learning-based automatic classification models for leukaemia detection using pictures of blood microscopy. The second model outperformed the first due to its 100% classification accuracy, as shown by experiments carried out on a dataset of 2820 photos.

In 2020, **Kumar et al. [44]** provided a dependable approach to differentiate between Acute lymphoblastic leukemia (ALL) and Multiple Myeloma (MM) by using a convolutional neural network and the SN-AM dataset. An overall accuracy of 97.2% was better than that of more conventional machine learning methods like decision trees, naive Bayes, Random Forests (RF), and Support Vector Machines (SVMs).

In 2020, **Shlol et al. [45]** proposed a hybrid method that is more effective in classifying white blood cell leukaemia. The author retrieved characteristics from white blood cell (WBC) photos using VGGNet, a robust CNN architecture that was pre-trained on ImageNet. Consequently, statistically enhanced Salp Swarm Algorithm (SESSA) has the best classification error on the very first dataset (ALL-IDB2) according to the root mean square error (RMSE) values, followed by Statistically Enhanced Multi-Verse Optimization (SEMVO).

3.2 CNN and Ensemble Model Research

In 2019 **Wang et al. [46]** implemented single shot multibox detector as well as an incremental improved version of you only look once (YOLO), two remarkable detection of objects methods. The optimized mean average precision and accuracy are 93.10% and 90.09%, respectively, with an inference time of 53 milliseconds per image on an NVIDIA GTX1080Ti GPU.

In 2019, **Ahmed et al. [47]** presented an innovative method for diagnosing all subtypes of leukaemia via convolutional neural network (CNN) and microscopic blood cell images. Experiments revealed that the efficacy of the CNN model in leukaemia versus health classification as well as multi-class classification across all subtypes is 88.25% and 81.74% accurate, respectively.

In 2019, **Liu and Long [48]** suggested using carefully selected training subsets to train an augmented picture ensemble for bagging. The combination of the ensemble model's predictions and the results from the preliminary and final tests yielded a weighted F1-score of 0.84 along 0.88, respectively. The model achieved results that put it in the best 10% within the ISBI-2019 categorization of Healthy vs Malignant White Blood Cells having Cancer competition.

In 2019, **Shekar and Dagnew [49]** recommended employing grid search-based hyperparameter tuning (GSHPT), a hyperparameter tuning approach based on grid search, to classify microarray cancer data via random forest parameters. Grid searches using n-fold cross-validation benefit most from using a constant set of parameter values. Two datasets—MLL and 3-class Leukemia—achieved test accuracy of 0.97, whilst Ovarian and SRBCT achieved 100%.

4. Research Gap

This section provides the research gap of the study.

- The availability of comprehensive datasets representing diverse blood cancer types, disease stages, and patient demographics is limited, hindering model generalization and performance.
- Deep learning models often lack interpretability, posing challenges in understanding how decisions are made and limiting their clinical adoption and trust among healthcare professionals.
- Models need to be robust to variations in image quality, staining techniques, and disease presentation, ensuring consistent performance across different clinical settings.
- Addressing the transferability of models across diverse populations with varying genetic backgrounds and environmental exposures to ensure equitable and accurate diagnosis.
- Exploration of longitudinal data and development of predictive models that could anticipate disease progression and treatment response for personalized management strategies.

5. Problem statement

The early detection and classification of blood cancer using deep learning approaches presents several significant challenges. One key issue is the scarcity of large, well-annotated datasets specific to blood cancer subtypes, which hinders the development and validation of robust deep-learning models. Another challenge lies in the interpretability of deep learning algorithms, particularly in medical contexts, where clinicians require transparency in decision-making processes for trust and adoption. Additionally, the heterogeneity of blood cancer manifestations across patients poses a challenge to model generalization and performance consistency.

The integration of deep learning-based diagnostic tools into clinical workflows requires addressing regulatory and ethical considerations to ensure patient safety and data privacy. Furthermore, the validation of deep learning models through rigorous clinical trials to demonstrate real-world effectiveness and reliability is essential. Overcoming these challenges is crucial for harnessing the potential of deep learning in revolutionizing blood cancer diagnosis, enabling earlier interventions, personalized treatments, and improved patient outcomes.

6. Objective

- To develop deep learning models for automated screening of blood cell images to detect early signs of leukaemia, lymphoma, and myeloma.
- To investigate transfer learning techniques to leverage pre-trained models for efficient feature extraction from limited annotated datasets.
- Enhance model interpretability by incorporating attention mechanisms and visualization techniques to identify critical diagnostic features.
- To validate deep learning models through large-scale clinical trials to assess performance, reliability, and impact on patient outcomes.

7. Research methodology.

In this part, the study will go over the general approach that was used when creating the model. The process begins with dataset selection, followed by data preprocessing involving resizing, normalization, and augmentation. Feature extraction is performed using the SIFT approach, and then feature selection is conducted using PCA. The data is split into training and testing sets. Next, a deep learning-based classification model, DenseNet-165 + ResNet-50, is applied for blood cancer detection. The model is trained on the prepared dataset. Finally, detection and performance evaluation are carried out to assess the effectiveness of the DenseNet-165 + ResNet-50 model in identifying blood cancer, ensuring robustness and accuracy in classification tasks.

7.1 Technique used.

This section provides a brief description of the technique used in the design and development of the deep learning model.

- **SIFT**

The Scale-Invariant Feature Transform (SIFT) technique is used for feature extraction in image processing and computer vision. In the context of blood cancer detection, SIFT extracts distinctive features from microscopic images of blood cells, such as shape and texture details, irrespective of scale and orientation variations. These extracted features are crucial for differentiating between healthy and abnormal cells [50]. By applying SIFT, relevant features are identified and utilized to train machine learning models like DenseNet-165 and ResNet-50, enabling accurate classification of blood cell images to detect signs of cancer-based on distinct visual patterns and characteristics.

This approach enhances the sensitivity and specificity of cancer detection algorithms in medical imaging applications [51].

- **Principal component analysis (PCA)**

PCA is used in blood cancer diagnosis as a dimensionality reduction approach. Here, PCA aids in the identification of biomarkers or important features linked to blood cancer using gene expression or medical imaging datasets [52]. PCA simplifies complicated data structures by reducing the data to a space with fewer dimensions while keeping the most beneficial components. Machine learning methods such as DenseNet-165 + ResNet-50 might use these reduced characteristics as input and improve the model's capacity to distinguish between non-cancerous and malignant samples using the found discriminating features. Therefore, PCA can enhance blood cancer detection models' efficiency and accuracy by zeroing in on pertinent data properties [53].

- **DenseNet-169**

The tightly linked layers of DenseNet-169 make it a famous convolutional neural networks (CNN) design more effective training and maybe better performance are outcomes of this dense connection architecture, which promotes feature reuse and improves gradient flow [54]. For blood cancer detection, DenseNet-169 is used as part of a deep learning model, possibly in conjunction with other networks like ResNet-50. The model learns to detect subtle patterns and features indicative of blood cancer from medical images, leveraging the powerful representation learning capabilities of DenseNet-169 to achieve accurate classification of cancerous and non-cancerous cells or tissues. This approach enables robust and reliable automated detection of blood cancer from diagnostic images. Figure 4 shows the network architecture of the DenseNet-165 [55].

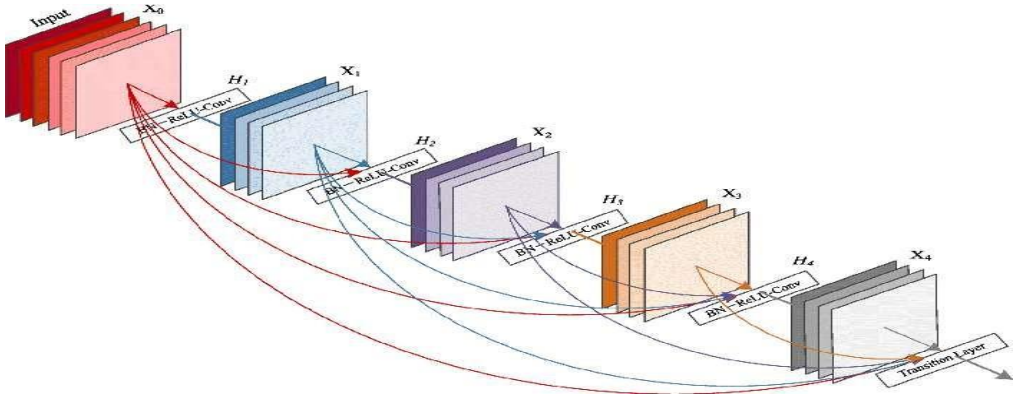

Figure 4. DenseNet network architecture [56].

- **ResNet-50**

The ResNet-50 architecture is a deep convolutional neural network that is composed of fifty layers. It is well-known for its ability to effectively handle difficult image recognition tasks. In the context of blood cancer detection, ResNet-50 is used as part of a hybrid model alongside DenseNet-165. This combination leverages the strengths of both architectures to accurately classify images related to blood cancer.

ResNet-50's deep layers enable it to learn intricate features from medical images, aiding in the identification of subtle abnormalities indicative of blood cancer [57]. By integrating ResNet-50 into the classification pipeline, the model could achieve high accuracy and sensitivity in detecting blood cancer based on extracted image features. Figure 5 represents the block diagram of ResNet-50.

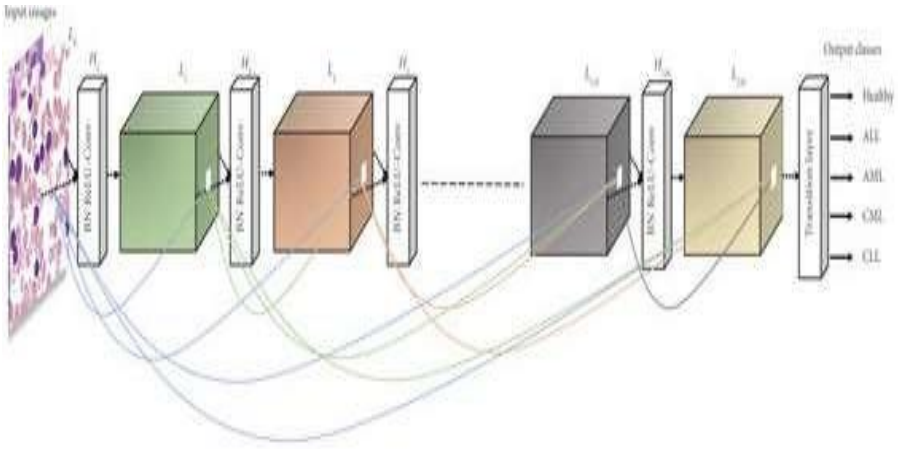

Figure 5. Architecture of ResNet-50 [58].

7.2 Proposed Architecture

This section provides the proposed architecture of the model in Figure 6.

Step 1: Dataset Selection:

The dataset Leukemia_GSE28497, which contains labelled medical images of blood samples with cancerous and non-cancerous cells, is selected.

Step 2: Data Preprocessing:

- **Resizing:** Resize all images to a uniform size for consistency.
- **Normalization:** Normalize pixel values to a standard scale (e.g., between 0 and 1).

$$Normalized_{Value} = \frac{Origina_value - \min_value}{\max_value - \min_value} \quad (1)$$

- **Augmentation:** Apply data augmentation techniques (e.g., rotation, flipping) to increase dataset diversity and robustness.

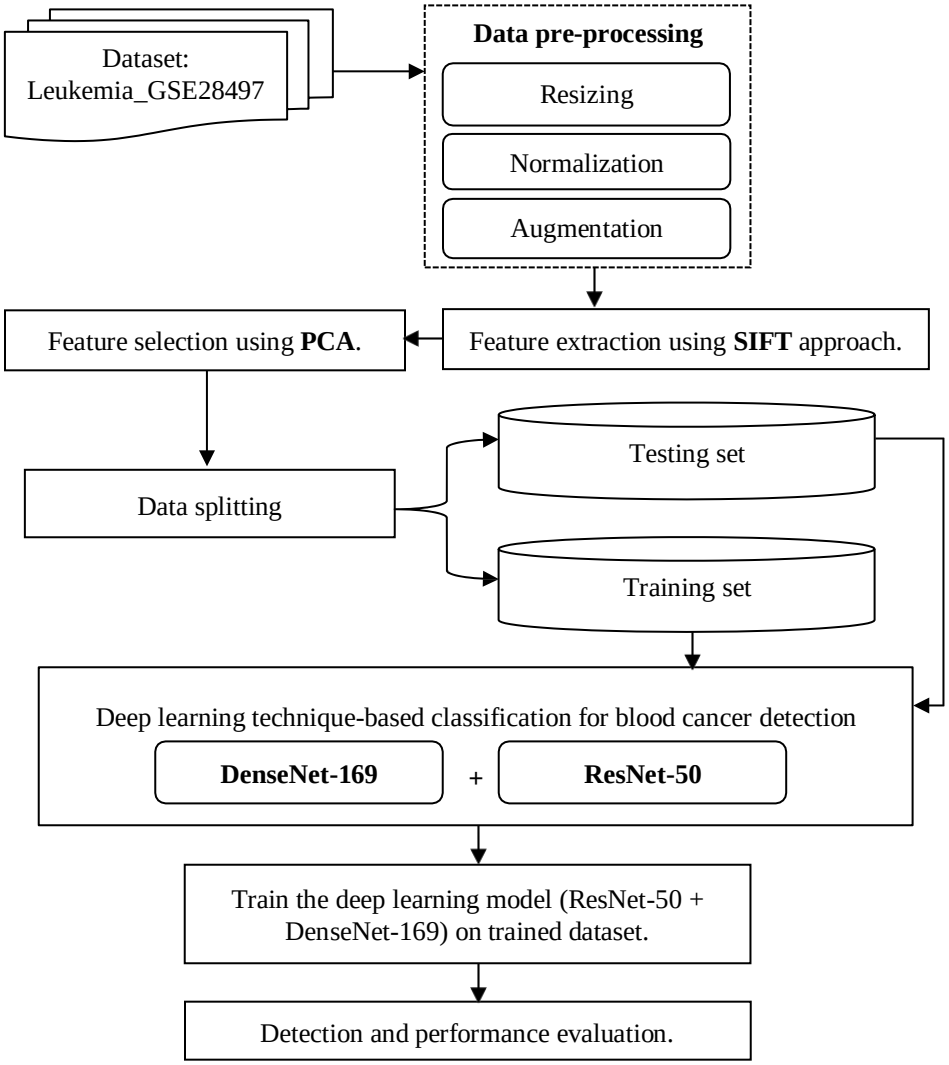

Figure 6. Proposed Architecture.

Step 3: Feature Extraction:

- Utilize the Scale-Invariant Feature Transform (SIFT) approach to extract distinctive features from preprocessed images.

Step 4: Feature Selection:

- Use Principal Component Analysis (PCA) to reduce the dimensionality of extracted features while preserving relevant information:

$$X_{pca} = X \cdot V \tag{2}$$

Where X is the feature matrix, and V contains the principal components.

Step 5: Data Splitting:

The dataset is divided into training and testing sets .

Step 6: Deep Learning Classification Model:

- Construct a hybrid deep learning model combining DenseNet-165 and ResNet-50 architectures:

$$Output_{model} = (Cojncatenate(DenseNet - 165(X), ResNet - 50(X))) \quad (3)$$

Where f is the activation function, and X represents the input image.

Step 7: Model Training:

- Train the hybrid model (DenseNet-165 + ResNet-50) on the training dataset:

$$Parameters_{opt} = argmin_{Parameters} Loss_{trai}(Parameters, Training_Data) \quad (4)$$

Step 8: Detection and Performance Evaluation:

- Apply the trained model to detect blood cancer in the testing dataset:

$$Predictions = Model_predic(Testing_data) \quad (5)$$

- Evaluate the model's performance using metrics like accuracy, precision, recall, and F1-score:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (6)$$

$$Precision = \frac{TP}{TP+FP} \quad (7)$$

$$Recall = \frac{TP}{TP+FN} \quad (8)$$

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (9)$$

- Analyze and interpret the results to assess the effectiveness of the deep learning-based blood cancer detection model.

8. Expected outcomes.

The expected outcome of research on deep learning approaches for early detection and classification of blood cancer includes the development of accurate and robust diagnostic models capable of identifying specific blood cancer types from diverse data sources such as blood smears, genetic sequences, or medical images. These models would enable earlier detection of blood cancer, leading to timely intervention and personalized treatment strategies. Additionally, the research aims to enhance the interpretability of deep learning models, providing insights into the underlying features driving diagnostic decisions. Successful implementation of these approaches has the potential to revolutionize hematologic cancer diagnostics, improving patient outcomes

through optimized treatment pathways and facilitating the integration of AI-driven tools into clinical practice for enhanced precision and efficiency in cancer care.

9. Chapter Plan

Chapter 1: The chapter introduces the research topic and describes the methods used, as well as the study's aims and rationale.

Chapter 2: This chapter presents a review of the previous studies that several authors provide.

Chapter 3: This chapter explains the methodology used in this research study. This chapter explores several stages of the methodology.

Chapter 4: This chapter explains how the results of the research study will be analyzed.

Chapter 5: This chapter provides a summary of this research effort, and numerous conclusions are formed based on the findings of this thesis's many investigations. A synopsis of the upcoming research activities is also provided.

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